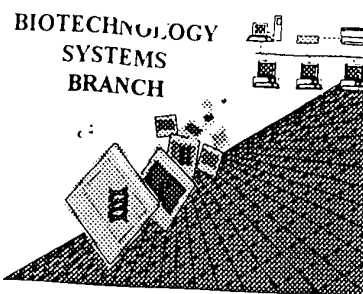


# RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/729,658A

Source: 1632

Date Processed by STIC: 5/4/2001

RECEIVED

MAY 21 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/729,658A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length  
Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8        Skipped Sequences (OLD RULES)  
Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)  
Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10   J   Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of "Artificial" (NEW RULES)  
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12        Use of <220>Feature (NEW RULES)  
Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1632

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:41

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Zonana et al.  
 5 <120> TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins  
 7 <130> FILE REFERENCE: 55924  
 9 <140> CURRENT APPLICATION NUMBER: 09/729,658A  
 10 <141> CURRENT FILING DATE: 2000-12-04  
 12 <150> PRIOR APPLICATION NUMBER: 09/342,681  
 13 <151> PRIOR FILING DATE: 1999-06-29  
 15 <150> PRIOR APPLICATION NUMBER: 60/092,279  
 16 <151> PRIOR FILING DATE: 1998-07-09  
 18 <150> PRIOR APPLICATION NUMBER: 60/112,366  
 19 <151> PRIOR FILING DATE: 1998-12-15  
 21 <160> NUMBER OF SEQ ID NOS: 122  
 23 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

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 2620 <211> LENGTH: 19  
 2621 <212> TYPE: DNA  
 2622 <213> ORGANISM: Artificial Sequence  
 2624 <220> FEATURE:  
 2625 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 2626 Oligonucleotide primers that can be used for  
 2627 mutation screening of human DL.  
 2629 <400> SEQUENCE: 93  
 2630 ctcgttggat ccttggcctt  
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 2750 <210> SEQ ID NO: 101  
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 2758 cctggccttg gtcccatccc acaaggagca gcatccagga cggagagtcc tggcccctcc 180  
 2759 ggtggacagg cagcccatca ggctctgcct ctgtgtctcc taagtggcca ttaaccatca 240  
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 E--> 2768 aatgcctata natcccataa gnntgcaggc tantgnggan ggtgctnaca aagagcatgt 780  
 E--> 2769 tcctcctcca ggaaggtctg gccttngttg gtgtnaccce tggggggcta ancaggccnt 840

see  
 item 10  
 on Error  
 Summary  
 Sheet

item 10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:42

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Output Set: N:\CRF3\05042001\I729658A.raw

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2772 tcaatattgt taaaagaatg ctccatttca agacaggctg aaaccccaag gaaactgagt 1020
2773 ggacagagca ggtgactgag tgggcgtggc ctcatgcccg acttgattgt gggcctgcag 1080
2774 actggccacc gtgctctctg caccagtccc tgccctgtgtg ctgtccagct cacctgtcta 1140
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2791 <213> ORGANISM: Homo sapiens
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2796 ctagtgaag tgctcctgtg gcctgtccag gcaggcttat gaaggaggag gcgtttgcca 180
2797 catctgagcc ttgagtcaga ggtcgagggt ctagtgcagg ttggccacca gctacctgac 240
E--> 2798 aagtcaacta acctccatga gcctcggtt tctcatcggg aatatggggg tgaagaaagn 300
E--> 2799 acaatanca tgactcttta gggttcatta aacagtctaa gaaatacaaa tatttagctc 360
2800 ccctcagcca tcaactgcctc agggccattc atgatcatga atccagatcc atgagctctg 420
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2823 ctccctaata taattgaatg acatgttgcc ccccgctgcag gaagtcatta tatctgcaat 180
2824 cagagttgat ccctctatgg gtgtcctggg accgctggga ggtgctgggt gtgaaggcgg 240
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E--> 2826 gcgtcctggg ctttgggttg gccgngagtt aacagcaatt ctatcactgg tttcatata 360
E--> 2827 aacatgctga ccatagcact ttaatatata cttgcanaan gtncaatttc attctncctt 420
E--> 2828 aaccagggaa gangggatcg nggaggaccc caangtttan tntgcctctc acanttagnc 480
E--> 2829 cccacantgg cttgncntna aggttgccaa agcagtagna gcgagaagca agctccctta 540
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2832 taagcaagca cctcagattt cagggttccc tgaaagcatc ccaggggag ggccattgct 720
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2876 cgtgggggtg tgccacacag acaccgggca gctctgcca acaggaagag cagggttggg 180
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:42

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

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E--> 2904 atttggtgcc tactgccac caagtgcctg gctaggcctg tgaacacatc ctnccttcca 480
E--> 2905 ccagcccang agcaagggtc ttggaatcat ccctggttat aggaatacca cactgaggta 540
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2910 gacaccagtt gaactgggt gcttactggg attaaatata gagatctagg acatattcaa 840
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2926 ggagcccgcc cctgacaagc agggctcccc ggagctgtgc ctgctgtgc tggttcacct 120
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2931 <211> LENGTH: 226
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2938 aagataggag acctggacag tgacaagttc acagcaagat agtcaaaagg gaaaaaac 180
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Item 10

Item 10

Item 10

Item 10

Item 10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:42

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

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2985 tagaaaacgt taatagaagt tctaagcggg agatgactcc ctactggat gatgaaggat 840
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3005 ttaacaccaa caagcaattt cccaccaacg aatgtagtac atactgtgag aggatcataa 2040
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Item 10

Item 10

Item 10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:42

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

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3014 atgggattca gaacaatgag atcataataa ttctcactga ccaaagctgg gactccatcc 2580
3015 tgccattttt gtgtggagat attcataatt ctgcaatact ttaaaacatt tagaaaacac 2640
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3093 <212> TYPE: DNA
3094 <213> ORGANISM: Artificial Sequence
3096 <220> FEATURE:
3097 <223> OTHER INFORMATION: Description of Artificial Sequence:
3098     Oligonucleotide primer that can be used to amplify
3099     TNF homology domain of mouse dl.
3101 <400> SEQUENCE: 122
3102 aagcttctag gatgcagggg c
E--> 3103 1
E--> 3106 55

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*delete at end of file*

21

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:43

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43  
L:2629 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:93  
L:2633 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 4 thru 93  
L:2662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95  
L:2663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95  
L:2664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95  
L:2667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95  
L:2698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97  
L:2699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97  
L:2700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97  
L:2761 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101  
M:340 Repeated in SeqNo=101  
L:2798 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103  
M:340 Repeated in SeqNo=103  
L:2826 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:105  
M:340 Repeated in SeqNo=105  
L:2877 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:109  
L:2898 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:111  
M:340 Repeated in SeqNo=111  
L:2925 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:112  
L:2939 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:113  
L:2958 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:115  
M:340 Repeated in SeqNo=115  
L:2980 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:116  
M:340 Repeated in SeqNo=116  
L:3103 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:21 SEQ:122  
M:254 Repeated in SeqNo=122